

FIG. 1

BLASTP - alignment of 359_protein (SEQ ID NO:2) against
swiss|Q05017|PHLX_RABIT PHOSPHOLIPASE ADRAB-B PRECURSOR (EC
3.1.-.-).//:treml|Z12841|OCPHILIP_1

product: "Phospholipase"; O.cuniculus mRNA for phospholipase.

//:gp|Z12841|1690 product: "Phospholipase"; O.cuniculus mRNA for
phospholipase.

This hit is scoring at : 0.0 (expectation value)
Alignment length (overlap) : 1217
Identities : 77 %
Scoring matrix : BLOSUM62 (used to infer consensus pattern)
Database searched : nrdb

Q: 1 EAWNSLLASSRYSEQESFTTVVFQPPFFYEETPSLHSEDPRLQDSTTLAWHLWNRMMEPAGE
EAW:SLLASS:Y:.QESF.VVFQPPFFYE:: S. :P LQD.TTLA .LWNRMMEP.G.
H: 259 EAWDSLLASSKYNTQESFAVVFQPPFFYESSLSALLAEPPLQDPTTLALSLWNRMMEPIGR

KDEPLSVKHGRPMKCPSESPLYFSYRNSNYLTRLQKPDKLGEKSIFLISLCVSFQVRE
K:EP.S K. :P::CP:QESPLYF:YRNS..LTR::PQ.KL :VRE
KEEPFSEKERKPLRCPTQESPLYFTYRNSGQLTRVSQPQGL-----EVRE

prosite signature

GAEIRCPDKDPSDVTPTSVMHRLKPADINVIGALGDSLTAGNGAGSTPGNVLDVLTQYRGL
G.EIRCPDKDPSD:VPTSVMHRLKPADI.VIGA:GDSLTAGNGAGS.PGN:LDVLTQYRGL
GTEIRCPDKDPSDVSPTSVMHRLKPADIKVIGAMGDSLTAGNGAGSQPGNILDVLTQYRGL

SWSVGGDENIGTVTTLANILREFNPSLKGFSVGTGKETSPNAFLNQAVAGGRAEDLPVQA
SWSVGGD:NI.TVTTLANILREFNPSL:GFSVGTG:ET::AF.NQAVAG.RA:.L QA
SWSVGGDQNIISTVTTLANILREFNPSLQGFSGVGTGRETTSQAFFNQAVAGARADGLIPQA

RRLVDLMKNDTRIHFQEDWKIITLFIGGNDLDCFCNDLVHYSQNFDTNIGKALDILHAE
:RLV LMKNDTRI:FQEDWKIIT:FIGGNDLDCFCND V.YSQNFDTNIG.ALDILHAE
QRLVALMKNDTRINFQEDWKIITVFIGGNDLDCFCNDPVRYSPQNFDTNIGTALDILHAE

VPRAFVNVLVTLEIVNLRELYQEKKVYCPMILRSLCPCVLKFDNDSTELATLIEFNKKF
:PRAFVNVLV.VLEI .LRELYQE.KV CPMILRSLCPCVLKFDNDSTE:A:LIE K::
IPRAFVNVLVKVLEISKRELYQETKVSCPMILRSLCPCVLKFDNDSTELASLIETIKEY

QEKTHQLIESGRYDTRDFTVVVQPPFFENVDMPKTSEGLPDNSFFAPDCFHFSKSHSRA
QE:T.QLI:SGRYDTR:DFTVV:QPPFE.V:MPKT.:GLPDNSFFAPDCFHFSK:H:.A
QERTQQLIDSGRYDTRDDFTVVLQPPFEKVMPKTQDGLPDNSFFAPDCFHFSKAKAHA

ASALWNNMLEPVGQKTTRHKFENKINITCPNQFFWSLSTLRFWDLFYALRGHGTWLPSCR
ASALWNNMLEPVGQKT::FE::NITCPNQ.: LST.: :G.GTWLPSCR
ASALWNNMLEPVGQKTTHNDFEGAVNITCPNQVWPFLSTYK-----NSVQGFGTWLPSCR

prosite signature

RAPSALHPTSVHALRPADIQVVAALGDSLTAGNGIGSKPDDLDPVTTQYRGLSYSAGGDG
R:PSA PTVHALRPADIQVVAALGDSLTAG GIGSKP:DL.D TTQYRGLSYS:GGDG
RSPSASPPTSVHALRPADIQVVAALGDSLTAGIGIGSKPNDLSDGTTQYRGLSYSAGGDG

SLENVTTLPNILREFNRNLTGYAVGTGDANDTNAFLNQAVPGAKAEDLMSQVQTLQMKMK
SL:NVTTLNPNILR:FN.NL.G:AVGTGDA:.TNAF.NQAVPGAKA.DLMSQVQTL:Q:MK
SLDNVTTLNPNILRQFNSNLMGFAVGTGDASGTNAFFNQAVPGAKARDLMSQVQTLVQRMK

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FIG. 2.

Prosites search result

Access#	From->To	Name	Doc#
PS00016	1096->1099	RGD	PDOC00016
PS01098	150->161	LIPASE_GDSL_SER	PDOC00842
PS01098	502->513	LIPASE_GDSL_SER	PDOC00842

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BOOKS BY

RIHFQEDWKIITLFIGGNDLCDFCND	277
R . Q:D .::T: :GGNDLCD: .D	
rkksqkdpdlvtielGgNDlcdyfrd	146

FIG. 4.

HMMPFAM - alignment of 359_protein (SEQ ID NO:2) against
pfam|hmm|Lipase_GDSL Lipase/Acylhydrolase with GDSL-like m

This hit is scoring at : 172.2 Expect: 8.7e-48

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Q: 501 VVAALGDSLTAGNGIGSKPDDLDPVTTQYRGLSYSAGGDSLENTTLPNILREFNRNLT
V.ALGDSLT G.G GS:...L.D .QYRGLS S: GDG:...N T.LP:IL.:
H: 1 kvvalGDSLtdggngsestklkdnyrqyrglspssvgdgnfsngtvlpdilakalgikl

G-----YAVGTGDANDTNAFLNQAVPGAEDLMSQVQTLNQ-----KMKDDH
G :.VG. .N.: . LN AV GA.AEDL:.....L:. KM ...
gVgikeksilfrvgklqengsltglnfAvgGataedllkrlpnlldqvikkssykmgyks

RVNFHEDWKVITVLIGGSDLCDYCTD 629
R . .:D .:T: :GG:DLCDY .D
rkksqkdpdlvtielGgNDlcdyfrd 146

5023845.101000

FIG. 5

HMMPFAM - alignment of 359_protein (SEQ ID NO:2) against
pfam|hmm|Lipase_GDSL Lipase/Acylhydrolase with GDSL-like m

This hit is scoring at : 155.2 Expect: 1.1e-42

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Q: 857 VVAALGDSLTVSMGARPNN--SSDLPTSWRGLSWSIGGDGNLEHTTLEPNILKKFNPYLL
V.ALGDSL.T.G...D...:RGLS.S.GDGN...T.LP:IL.K.L
H: 1 kvvalGDSLtdggngsestklkdnyrqyrglspssvgdgnfsngtvlpdilakalgikl

G-----FSTSTWEGTAGLNVAEGARARDMPAQAWDLVE-----RMKNSP
G.....GLN.A.GA.A.D:...:L:::M...
gVgikeysilfrvgklqengsltglnfAvgGataedllkrlpnlldqvikksgykmygks

DINLEKDWKLVTLFIGVNDLCHYCEN 980
. :KD.LVT: :G NDLC.Y :
rkksqkdpdlvtielGgNDlcdyfrd 146

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SEQUENCE LISTING

SEQ ID NO:1

gaagcctgga acagcctcct ggcctccagc aggtacagtg agcaggagtc cttcacctg
gttttccagc ctttcttcta tgagaccacc ccatctctac actcggagga cccccgactc
caggattcta ccacgctggc ctggcatctc tggaatagga tgatggagcc agcaggagag
aaagatgagc cattgagtgt aaaacacggg aggccaatga agtgtccctc tcaggagagc
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acactgcccc acattctgaa gaagttcaac ccttacctcc ttggcttctc taccagcacc
tgaggaggga cagcaggact aaatgtggca gcggaagggg ccagagctag ggacatgcc
gccaggcct gggacctggt agagcgaatg aaaaacagcc ccgacatcaa cctggagaaa
gactggaagc tggtcacact cttcattggg gtcaacgact tgtgtcatta ctgtgagaat
ccggaggccc acttgccac ggaatatgtt cagcacatcc aacaggccct ggacatcctc
tctgaggagc tccaagggc ttctgtcaac gtggtggagg tcatggagct ggctagcctg
taccagggcc aaggcgggaa atgtgccatg ctggcagctc agaacaactg cacttgccctc

SEQ ID NO:2

EAWSLLASS RYSEQESFTV VFQPFYETT PSLHSEDPR L QDSTTLAWHL WNRMMEPAGE
KDEPLSVKHG RPMKCPSQES PYLFSYRNSN YLTRLQKPQD KLGEKSIFLI SLCVSFQVRE
GAEIRCPDKD PSDTVPTSVH RLKPADINVI GALGDSLTA NGAGSTPGNV LDVLTQYRGL
SWSVGGDENI GTVTTLANIL REFNP SLKGF SVGTGKETSP NAFLNQAVAG GRAEDLPVQA

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GCCAGGCTGGAGGCCTTCAGCCGAGCCTACCGGAGCAGCATGCGCGAGCTGGTGGGGTCA
GGCCGCTATGACACGCAGGAGGACTTCTCTGTGGTGCTGCAGCCCTTCTTCCAGAACATC
CAGCTCCCTGTCTTGGCGGATGGGCTCCCAGATACGTCCTTCTTTGCCCCAGACTGCATC
CACCCAAATCAGAAATTCCACTCCCAGCTGGCCAGAGCCCTTTGGACCAATATGCTTGAA
CCACTTGGAAGCAAAACAGAGACCCTGGACCTGAGAGCAGAGATGCCCATCACCTGTCCC
ACTCAGAATGAGCCCTTCTGAGAACCCTCGGAATAAGAACTACACGTACCCCATCAAG
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GGTCCAAT

SEQ ID NO:6
embl|AA418228|HS1213659 . (EST)
CCCAGCTGGCAGAGCCTTTGGACCAATATGCTTGAACCACTTGAAGCAAAACAGAGACC
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AACCCTCGGAATAGTAACTACACGTACCCCATCAAGCCAGCCATTGAGAACTGGGGCAGT
GACTTCTGTGTACAGAGTGGAAGGCTTCCAATAGTGTTCACCTCTGTCCACCAGCTC
CGACCAGCAGACATCAAAGTGGTGG

SEQ ID NO:7
embl|AI952246|AI952246 . (EST)
TAAATAGCTTTGGACTTTATTTAAATGTATCCATTCCAGGAGCATAGGCCTGGAAGAAG
CCCAGGCCCCAAGAAGTTGTGACTGTCCCCTGGGCTTCTAGGGCACCAGGCATTGAAGC
ATGTCCTGGTGGCCGGGAGTGGCTGGGGCAGAGGGCGGTGAAGAGGGTGGCTATAGGGAG
TTTAGGGTGAGGACCCACCCCGGGCCTAGAGGGCCACAGTGCGCAGGCTCATTGGAGGA
TCTTCCCTCCGGCCACCTCTCTGCACCTCCAGACCACTGTCCCGATGATGCCCAACACA
AGGCCGACTCCCGCTGCCACTGGGACAGCCAGTAGAGCACCTCGGGGGCTTCTTCAGCC
TGGTCTGGGAGCAGTCGGCTGTTCCGCAGGGTGTAGAGGTAAGGGCTCTCAGGAGAGNG
CACTTGAGTTGGCTCGGCTGTGGGT